



SEQUENCE LISTING

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FEB 22 2001

TECH CENTER 1600/2900

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Tezuka, Katsunari<120> CELL SURFACE MOLECULE MEDIATING CELL
ADHESION AND SIGNAL TRANSMISSION

<130> 06501-039001

<140> US 09/383,551

<141> 1999-08-26

<150> PCT/JP98/00837

<151> 1998-02-27

<150> JAPAN 09-62290

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Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc 144
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat 192
Gln Gln Phe Lys Met Gln Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg 240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta 288
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca 336
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110

 att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg 384
 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125

 cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc 432
 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140

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 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 145 150 155 160

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 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
 165 170 175

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 35 40 45
 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65 70 75 80
 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
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 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140
 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
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Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser																
10 15 20 25																
gcc aat tat gag atg ttt ata ttt cac aac gga ggt gta caa att tta																148
Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu																
30 35 40																
tgc aaa tat cct gac att gtc cag caa ttt aaa atg cag ttg ctg aaa																196
Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys																
45 50 55																
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Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn																
60 65 70																
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Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn																
75 80 85																
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Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn																
90 95 100 105																
tat tac ttc tgc aac cta tca att ttt gat cct cct cct ttt aaa gta																388
Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val																
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Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys																
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Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val																
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Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr																
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170 175 180 185																
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Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp Val Thr Leu
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gccttggtag	tgccgagtc	tctcaaaaca	aacaccctct	tgcaaccagc	tttggagaaa	862
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gtc	ttt	gtc	ttc	tgc	ttc	cta	atc	aaa	ctt	tta	aca	gga	gaa	ctc	aat	103
Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Asn	
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gac	ttg	gcc	aat	cac	agg	atg	ttt	tcg	ttt	cac	gat	gga	ggg	gta	cag	151
Asp	Leu	Ala	Asn	His	Arg	Met	Phe	Ser	Phe	His	Asp	Gly	Gly	Val	Gln	
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gccctggcac tttaagatag ccttctttag aacatgagtt agttggtagt attctgacgt 1944
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Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
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ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45

cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
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Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

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Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta 432
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

ccc gta ggg ttg cca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480
Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528
Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

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 Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
 10 15 20

gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag 151
 Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
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 Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
 40 45 50 55

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247
 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
 60 65 70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295
 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
 75 80 85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343
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 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
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 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
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ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 487
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 140 145 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535
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170	175	180	
atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt aca gca			631
Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Thr Ala			
185	190	195	
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Pro Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg			
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Asn			
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Gln Ile Ser Cys Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
35 40 45
Phe Lys Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly
50 55 60
Asn Thr Val Ser Ile Lys Asn Pro Met Cys Tyr Gln Leu Ser Asn Asn
65 70 75 80
Ser Val Ser Phe Phe Leu Asn Asp Ser Ser Gln Gly Ser Tyr Cys Ser
85 90 95
Leu Ser Ile Phe Asp Pro Pro Pro Phe Gln Glu Asn Leu Ser Gly Gly
100 105 110
Tyr Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
115 120 125
Pro Val Gly Cys Ala Ala Phe Val Leu Leu Phe Gly Cys Ile Ile Trp
130 135 140
Phe Lys Lys Lys Tyr Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met
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<210> 14
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<213> Homo sapiens

<400> 14

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Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
          35           40           45
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
          50           55           60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65           70           75           80
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
          85           90           95
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
          100          105          110
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
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His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
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Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145           150           155           160
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
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Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
          50           55           60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65           70           75           80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
          85           90           95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
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Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
          115          120          125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
          130          135          140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
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Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
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Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
          180          185          190
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 50 55 60
 Lys Ala Tyr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
 65 70 75 80
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr
 85 90 95
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
 115 120 125
 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175
 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
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 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
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 Cys Thr Tyr Gly Asn Val Lys Cys Gly Leu Ser Asn Asn Ser Val Phe
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 Leu Gln Asn Leu Thr Tyr Phe Cys Lys Glu Met Tyr Pro Pro Pro Tyr
 50 55 60
 Asn Gly Thr Ile His Val Leu Cys Pro Phe Trp Leu Val Leu Tyr Ser
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 Leu Thr Ala Ile Lys Lys Arg Ser Leu Gly Tyr Met Met Pro Pro Lys
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 Gln Pro Tyr Asp Phe

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 Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
 20 25 30
 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val

